In the Claims:

1. (Currently amended) An automated modeler for modeling of an interactive system comprising at least one biological entity and at least one pharmaceutical substance, the system comprising:

a representation of states of said system,

an input, associated with said representation for allowing users to define at least one of, said states, expected relationships between said states and independent inputs to said states,

a data miner associated with said representation to operate on data taken from said system to apply said data to said states in accordance with said defined relationships and inputs, thereby to apply numerical values to said relationships and said inputs, thereby to model ~~said~~ interactions within said system to provide a prediction for future states of said system.

2. (Original) A modeler according to claim 1, wherein said states include beneficial actions of said pharmaceutical substance.

3. (Original) A modeler according to claim 1, wherein said states include harmful actions of said pharmaceutical substance.

4. (Original) A modeler according to claim 1, said model being usable to predict harmful interactions of said pharmaceutical substance within said system.

5. (Original) A modeler according to claim 4, said interactions being between at least one biological entity and a plurality of pharmaceutical substances.

6. (Original) A modeler according to claim 4, said interactions being between at least one pharmaceutical entity and a plurality of biological entities.

7. (Original) A modeler according to claim 1, said data being clinical trial data.

8. (Original) A modeler according to claim 1, said model being usable to direct a clinical trial.

9. (Original) A modeler according to claim 1, said model being usable to direct drug administration to a patient.

10. (Original) A modeler according to claim 1, further operable to use a second data set to calibrate said model.

11. (Original) A modeler according to claim 1, further operable to use a third data set to test said model.

12. (Currently amended) An automated system for processing effects on liver toxicity of at least one pharmaceutical substance in application to a biological entity, the system comprising:

a representation of states of said application,

an input, associated with said representation for allowing users to define expected relationships between said states, and independent inputs to said states,

a data miner associated with said representation to operate on data taken from said application to apply said data in accordance with said defined relationships and inputs, thereby to apply numerical values to said ~~interactions~~ relationships and said inputs, to model said application to provide a prediction for future states of said application.

13. (Original) A system according to claim 12, said application comprising a plurality of pharmaceutical substances.

14. (Original) A system according to claim 12, said data being clinical trial data.

15. (Original) A system according to claim 12, usable to direct a clinical trial.

16. (Original) A system according to claim 12, usable to direct drug administration to a patient.

17. (Original) A system according to claim 12, further comprising a second data set usable to calibrate said model.

18. (Original) A system according to claim 12, further comprising a third data set usable to test said model.

19. (Currently amended) A system for predicting likely liver toxicity as a side effect of application of a pharmaceutical substance, the system comprising:

an input device for obtaining blood levels of ALT and AST respectively,

a comparator, associated with said input device for comparing said respective levels of ALT (alanine aminotranferase) and AST (aspartate aminotransferase) to produce a ratio of said levels, and

a predictor associated both with said input device and said comparator, and including a statistical model, for predicting, from application of said levels and said ratio therebetween to said statistical model, a likelihood of development of liver toxicity.

20. (Original) A system according to claim 19, said predictor set to conclude from low ALT and AST levels and a ratio close to 1, that a likelihood of development of liver toxicity is low.

21. (Original) A system according to claim 20, said predictor being set to conclude from high ALT and AST levels, that a likelihood of liver toxicity is relatively high.

22. (Original) A system according to claim 20, said predictor being set to conclude from a ratio not close to 1, that a likelihood of liver toxicity is relatively high.

23. (Original) A system according to claim 21, said predictor being set to conclude from a ratio close to 1, that a likelihood of liver toxicity is relatively low.

24. (Original) A system according to claim 20, further comprising a thresholder for setting a threshold likelihood, above which application of said pharmaceutical substance is to be discontinued.

25. (Currently amended) A method for modeling an interaction between at least one biological system and at least one pharmaceutical substance, the method comprising:

building a state diagram of states of said interaction,

entering at least one of inputs to said states and ~~interactions~~ relationships between said states,

defining at least one output from at least one of said states,

obtaining empirical data regarding said interaction,

carrying out data mining on said empirical data to assign at least one of values to said relationships and functions to said states, thereby to obtain a quantitative model of said interaction.

26. (Original) A method according to claim 25, comprising:

randomly dividing said empirical data set into at least two data sets,

performing said data mining using only one of said sets,

testing said model using a remaining one of said sets to ensure that said data has not been overfitted.

27. (New) A modeler according to claim 1, wherein said biological entity is a macro-biological entity.